In the Specification:

The paragraph, beginning at page 103, line 35 has been amended as follows:

--The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO317. In particular, cDNA encoding a PRO317 polypeptide has been identified and isolated, as disclosed in further detail in the Examples below. Using ~~BLAST™~~ BLAST and ~~FastA™~~ FastA sequence alignment computer programs, it was found that a full-length native-sequence PRO317 (shown in Figure 42 and SEQ ID NO:114) has 92% amino acid sequence identity with EBAF-1. Further, it is closely aligned with many other members of the TGF- superfamily.--

The paragraph, beginning at page 162, line 22 has been amended as follows:

--Based on ~~BLAST™~~ BLAST and ~~FastA™~~ FastA sequence alignment analysis (using the ~~ALIGN™~~ ALIGN computer program) of the full-length PRO317sequence, PRO317 shows the most amino acid sequence identity to EBAF-1 (92%). The results also demonstrate a significant homology between human PRO317 and mouse LEFTY protein. The C-terminal end of the PRO317 protein contains many conserved sequences consistent with the pattern expected of a member of the TGF- superfamily.--

The paragraph, beginning at page 195, line 33 has been amended as follows:

--Twelve micrograms of the desired plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents ~~Superfect~~ SUPERFECT® (Quiagen), ~~Dosper~~ DOSPER® or ~~Fugene~~ FUGENE® (Boehringer Mannheim). The cells were grown and described in Lucas *et al.*, supra. Approximately 3 x 10^{-7} cells are frozen in an ampule for further growth and production as described below.--

The paragraph, beginning at page 197, line 26 has been amended as follows:

--Recombinant baculovirus is generated by co-transfecting the above plasmid and ~~BaculoGold™~~ BACULOGOLD™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using ~~lipofectin~~ LIPOFECTIN® (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28°C, the released viruses are harvested and used for

further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., Baculovirus expression vectors: A ~~laboratory~~ Laboratory Manual, Oxford: Oxford University Press (1994).--

The paragraph, beginning at page 198, line 17 has been amended as follows:

--Following PCR amplification, the respective coding sequences were subcloned into a baculovirus expression vector (pb.PH.IgG for IgG fusions and pb.PH.His.c for poly-His tagged proteins), and the vector and ~~Baculogold®~~ BACULOGOLD® baculovirus DNA (Pharmingen) were co-transfected into 105 *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711), using ~~Lipofectin~~ LIPOFECTIN® (Gibco BRL). pb.PH.IgG and pb.PH.His are modifications of the commercially available baculovirus expression vector pVL1393 (Pharmingen), with modified polylinker regions to include the His or Fc tag sequences. The cells were grown in Hink's TNM-FH medium supplemented with 10% FBS (Hyclone). Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells in Hink's TNM-FH medium supplemented with 10% FBS at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days at 28°C. The supernatant was harvested and the expression of the constructs in the baculovirus expression vector was determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A SEPHAROSE™ ~~Sepharose~~ CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.--

The paragraph, beginning at page 207, line 6 has been amended as follows:

--PDB12 pancreatic ductal cells are plated on fibronectin coated 96 well plates at $1.5x10^3$ cells per well in 100 µL/180 µL of growth media. 100 µL of growth media with the PRO polypeptide test sample or negative control lacking the PRO polypeptide is then added to well, for a final volume of 200 µL. Controls contain growth medium containing a protein shown to be inactive in this assay. Cells are incubated for 4 days at 37°C. 20 µL of ~~Alamar Blue~~ ALAMAR BLUE™ dye (AB) is then added to each well and the flourescent reading is measured at 4 hours post addition of AB, on a microtiter plate reader at 530 nm excitation and 590 nm emission. The

standard employed is cells without Bovine Pituitary Extract (BPE) and with various concentrations of BPE. Buffer or CM controls from unknowns are run 2 times on each 96 well plate.--

The paragraph, beginning at page 207, line 14 has been amended as follows:

--These assays allow one to calculate a percent decrease in protein production by comparing the ~~Alamar Blue~~ ALAMAR BLUE™ Dye calculated protein concentration produced by the PRO polypeptide-treated cells with the ~~Alamar Blue~~ ALAMAR BLUE™ Dye calculated protein concentration produced by the negative control cells. A percent decrease in protein production of greater than or equal to 25% as compared to the negative control cells is considered positive.--

The paragraph, beginning at page 208, line 7 has been amended as follows:

--Percent increase in protein production is calculated by comparing the ~~Alamar Blue~~ ALAMAR BLUE™ Dye calculated protein concentration produced by the PRO polypeptide-treated cells with the ~~Alamar Blue~~ ALAMAR BLUE™ Dye calculated protein concentration produced by the negative control cells. A percent increase in protein production of greater than or equal to 25% as compared to the negative control cells is considered positive.--

The paragraph, beginning at page 222, line 33 has been amended as follows:

--The starting material for the screen was genomic DNA isolated from a variety cancers. The DNA is quantitated precisely, *e.g.*, fluorometrically. As a negative control, DNA was isolated from the cells of ten normal healthy individuals which was pooled and used as assay controls for the gene copy in healthy individuals (not shown). The 5' nuclease assay (for example, ~~TaqMan™~~ TAQMAN™) and real-time quantitative PCR (for example, ~~ABI Prizm 7700 Sequence Detection System™~~ ABI PRIZM 7700 SEQUENCE DETECTION SYSTEM™ (Perkin Elmer, Applied Biosystems Division, Foster City, CA)), were used to find genes potentially amplified in certain cancers. The results were used to determine whether the DNA encoding the PRO polypeptide is over-represented in any of the primary lung or colon cancers or cancer cell lines or breast cancer cell lines that were screened. The primary lung cancers were obtained from individuals with tumors of the type and stage as indicated in Table 8. An

explanation of the abbreviations used for the designation of the primary tumors listed in Table 8 and the primary tumors and cell lines referred to throughout this example are given below.--

The paragraph, beginning at page 222, line 44 has been amended as follows:

--The results of the ~~TaqMan™~~ TAQMAN™ are reported in delta (Δ) Ct units. One unit corresponds to 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold, 3 units to 8-fold amplification and so on. Quantitation was obtained using primers and a ~~TaqMan™~~ TAQMAN™ fluorescent probe derived from the PRO polypeptide-encoding gene. Regions of the PRO polypeptide-encoding gene which are most likely to contain unique nucleic acid sequences and which are least likely to have spliced out introns are preferred for the primer and probe derivation, *e.g.*, 3'-untranslated regions. The sequences for the primers and probes (forward, reverse and probe) used for the PRO polypeptide gene amplification analysis were as follows:--

The paragraph, beginning at page 226, line 11 has been amended as follows:

--The 5' nuclease procedure is run on a real-time quantitative PCR device such as the ~~ABI Prizm 7700 Sequence Detection System™~~ ABI PRIZM 7700 SEQUENCE DETECTION SYSTEM™. The system consists of a thermocycler, laser, charge-coupled device (CCD) camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.--

The paragraph, beginning at page 229, line 26 has been amended as follows:

--The fluorometricly determined concentration was then used to dilute each sample to 10 ng/μl in ddH_2O. This was done simultaneously on all template samples for a single ~~TaqMan™~~ TAQMAN™ plate assay, and with enough material to run 500-1000 assays. The samples were tested in triplicate with ~~TaqMan™~~ TAQMAN™ primers and probe both B-actin and GAPDH on a single plate with normal human DNA and no-template controls. The diluted samples were used provided that the CT value of normal human DNA subtracted from test DNA was +/- 1 Ct.

The diluted, lot-qualified genomic DNA was stored in 1.0 ml aliquots at -80°C. Aliquots which were subsequently to be used in the gene amplification assay were stored at 4°C. Each 1 ml aliquot is enough for 8-9 plates or 64 tests.--

The paragraph, beginning at page 237, line 4, has been amended as follows:

--Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm^2 in Ham F-12 containing 10% FBS and 4 μg/ml gentamycin. The culture media is changed every third day and the cells are reseeded to 25,000 cells/cm^2 every five days. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100μl of the same media without serum and 100 μl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 μl/well. After 5 days at 37°C, 20 μl of ~~Alamar Blue~~ ALAMAR BLUE™ Dye is added to each well and the plates are incubated for an additional 3 hours at 37°C. The fluorescence is then measured in each well (Ex:530 nm; Em: 590 nm). The fluorescence of a plate containing 200 μl of the serum-free medium is measured to obtain the background. A positive result in the assay is obtained when the fluorescence of the PRO polypeptide treated sample is more like that of the positive control than the negative control.--

The paragraph, beginning at page 248, line 9, has been amended as follows:

--The following materials have been deposited with the American Type Culture Collection, ~~12301 Parklawn Drive, Rockville, MD,~~ 10801 University Boulevard, Manassas, VA USA (ATCC):

Please replace the paragraph beginning at page 249, line 22, with the following rewritten paragraph:

--These deposit were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations there under (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by

ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures that all restrictions imposed by the depositor on the availability to the public of the deposited material will be irrevocably removed upon the granting of the pertinent U.S. patent, assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).--